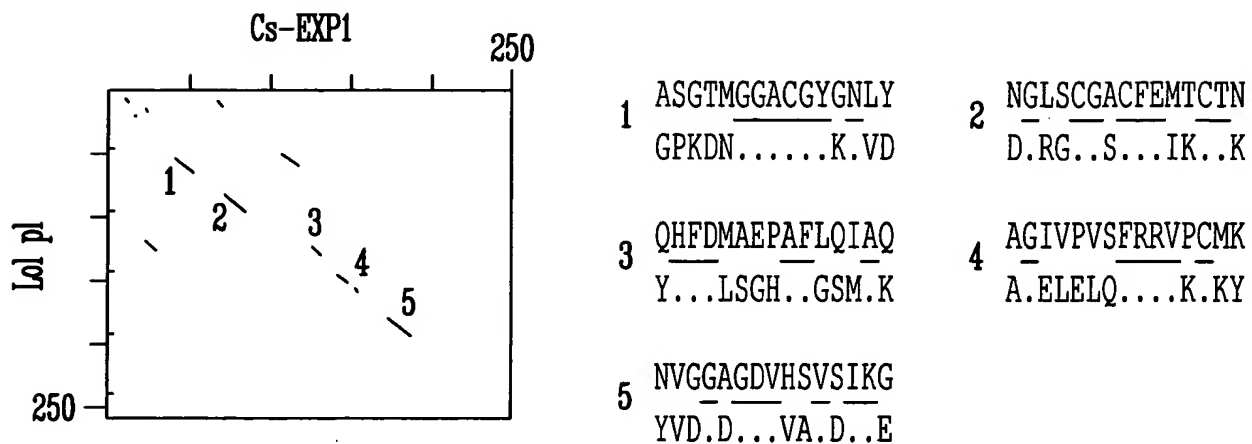
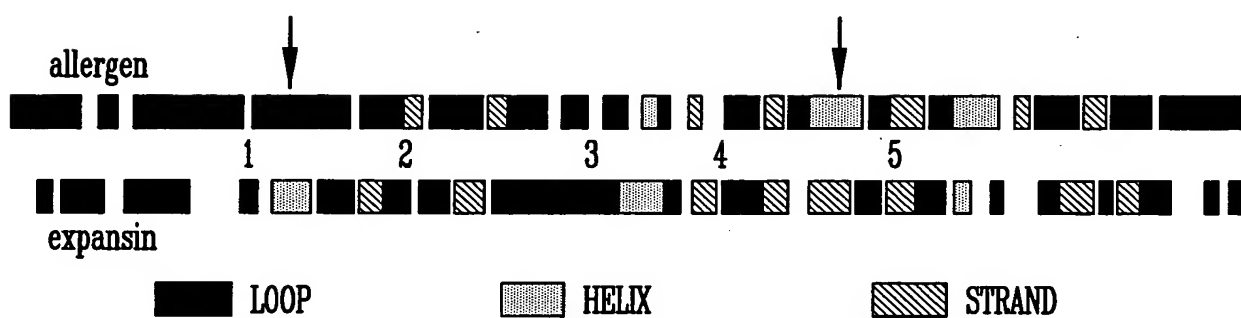


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*Fig. 1A**Fig. 1B*

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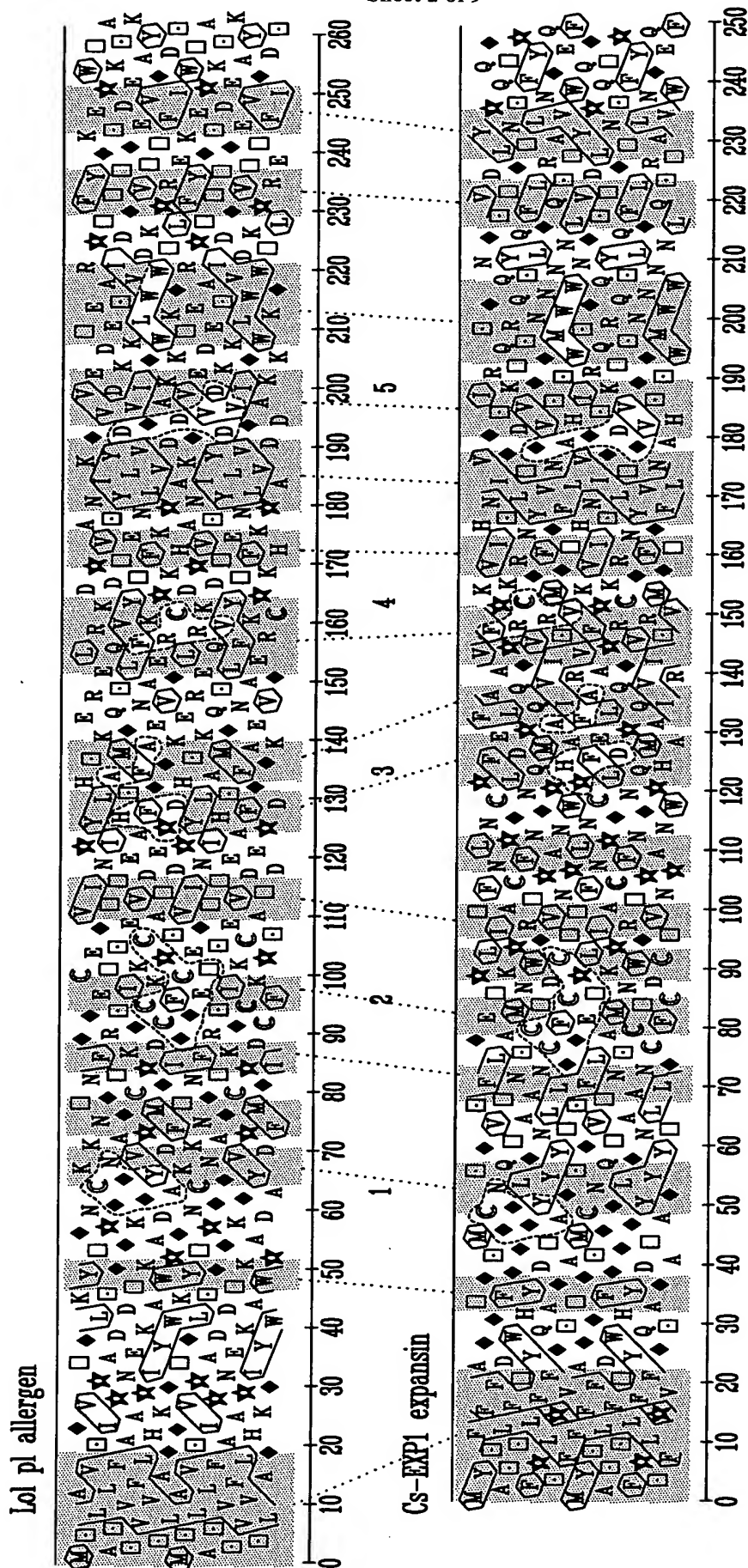


Fig. 1C

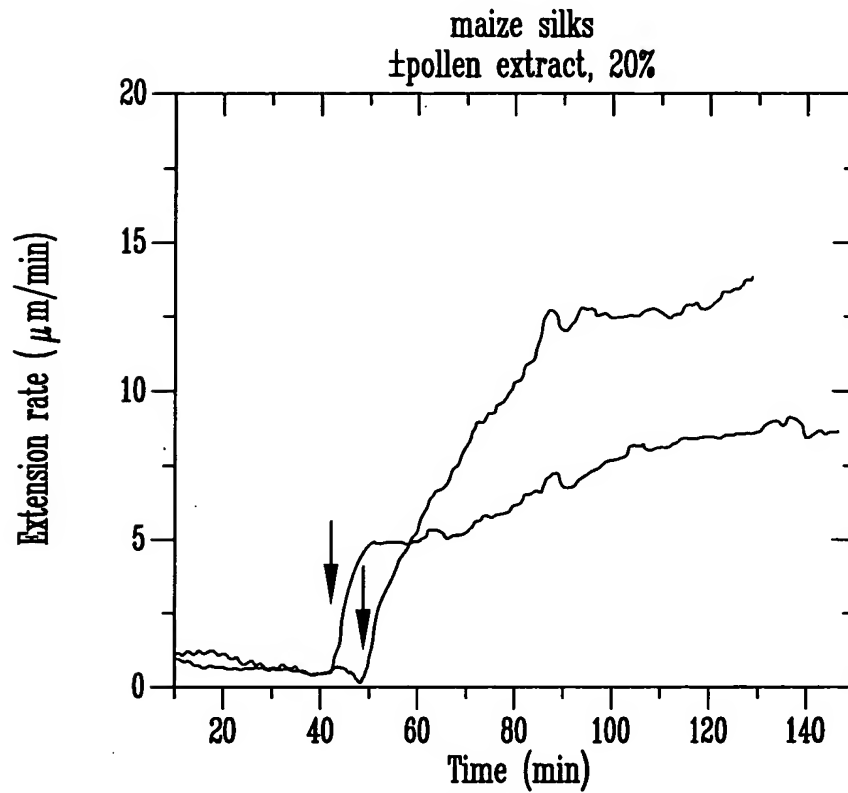


Fig. 2A

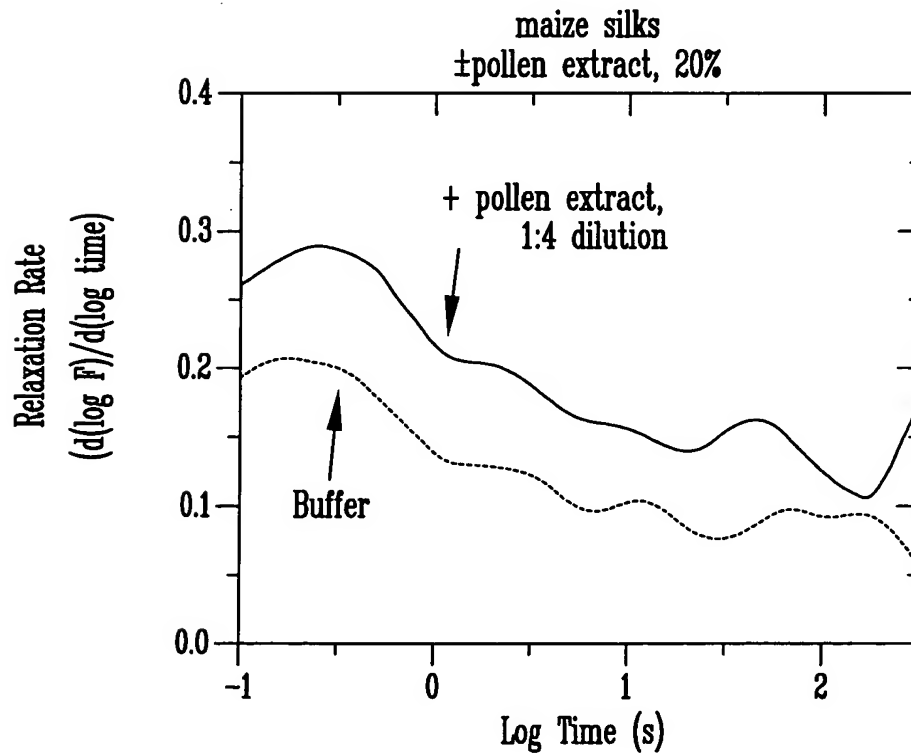
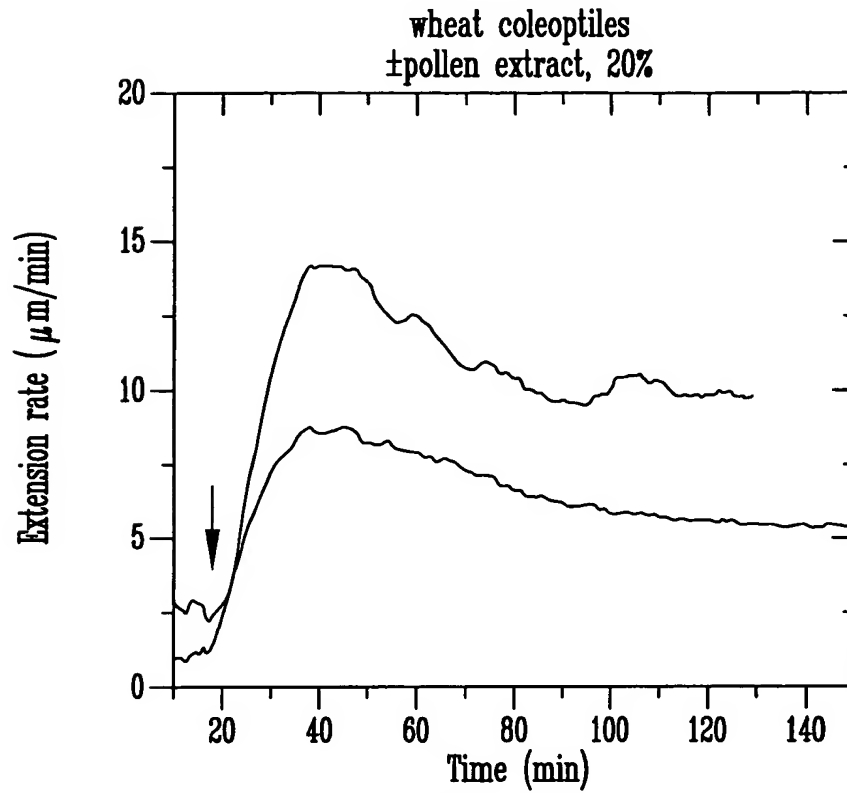
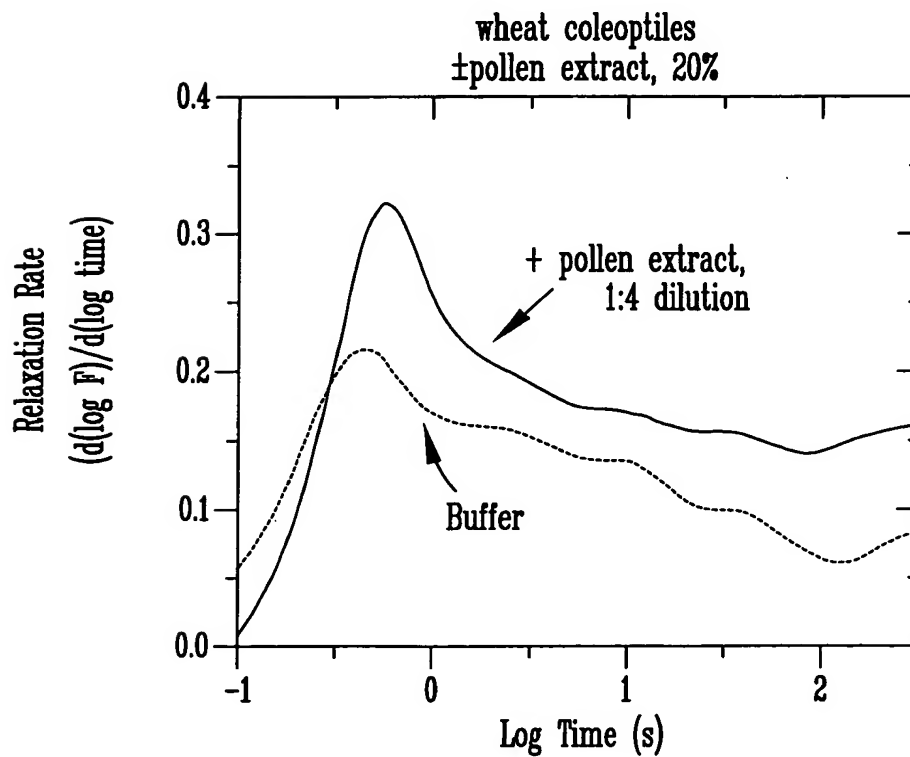


Fig. 2B

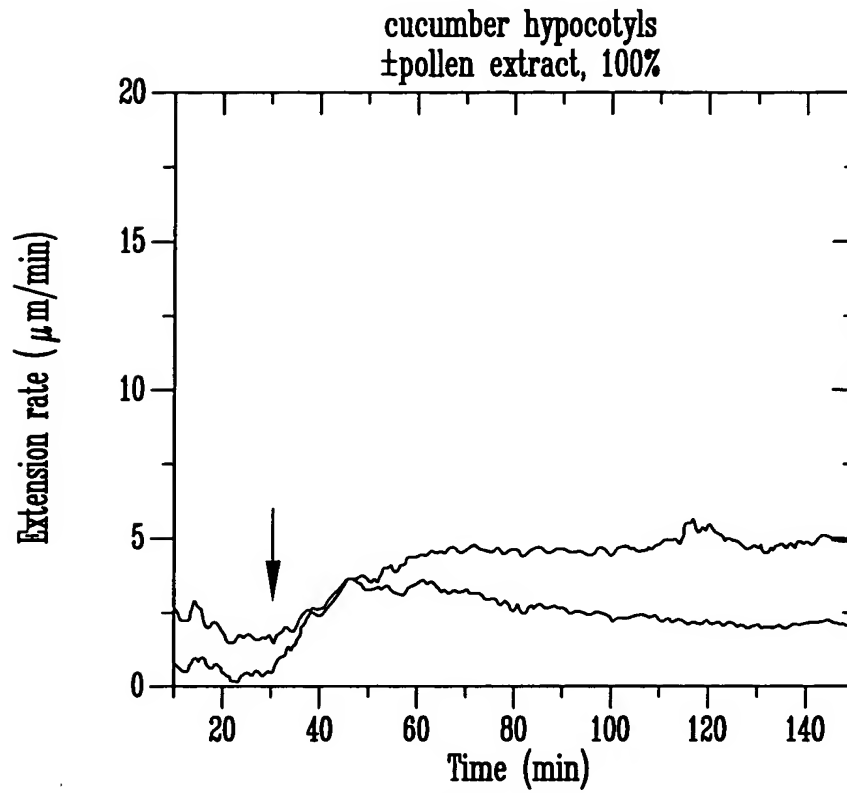
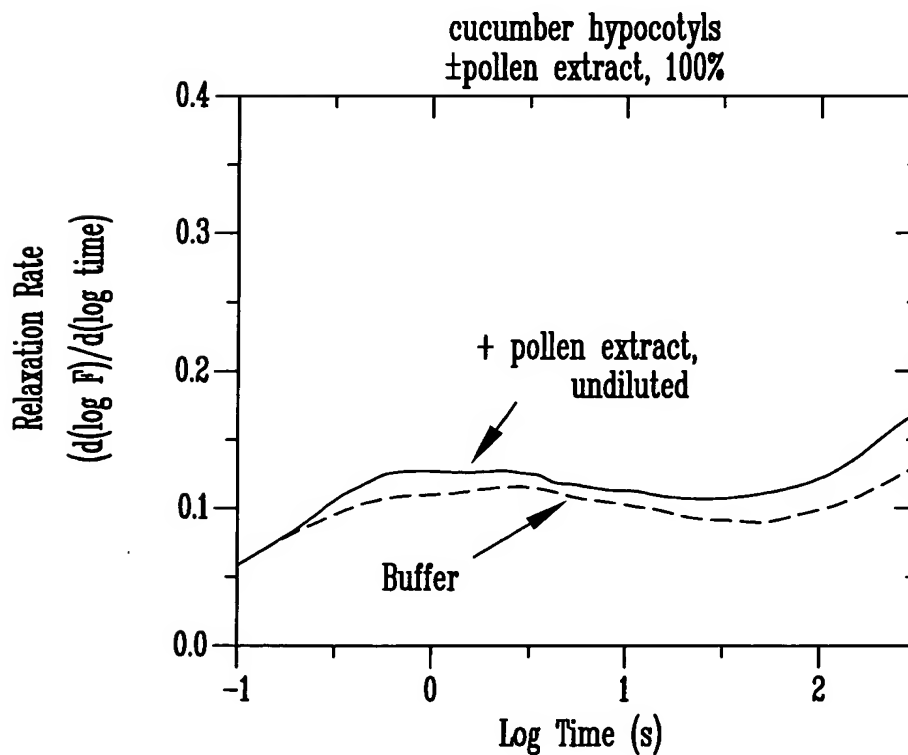
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*Fig. 2C**Fig. 2D*

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*Fig. 2E**Fig. 2F*

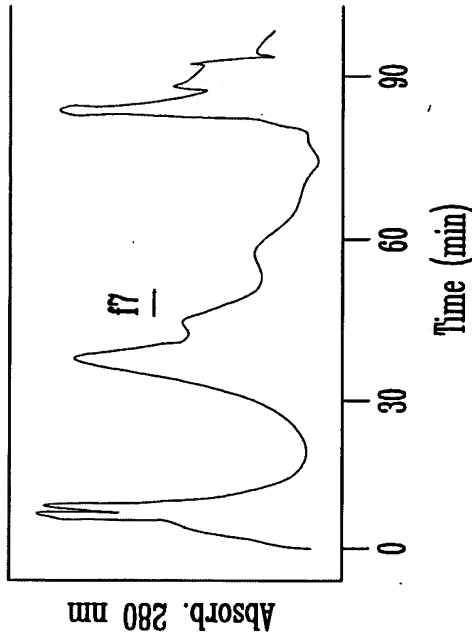


Fig. 3D

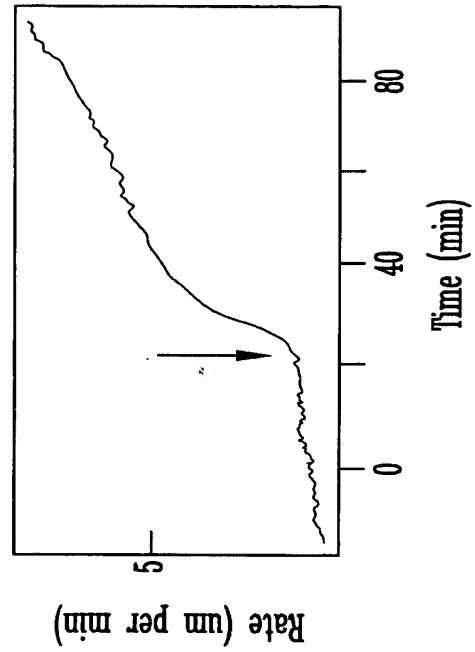


Fig. 3C

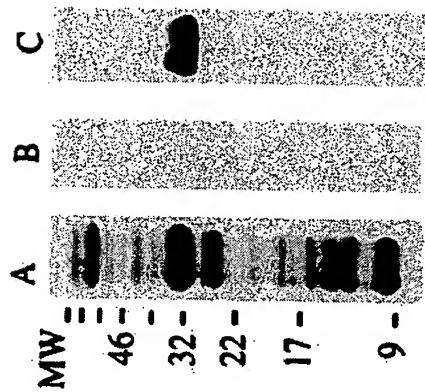


Fig. 3A,B,C

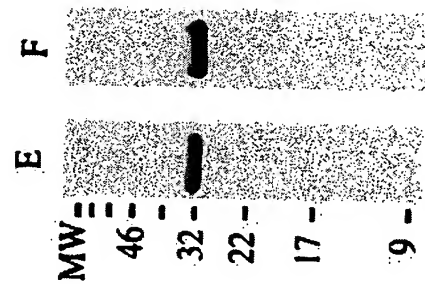


Fig. 3E,F

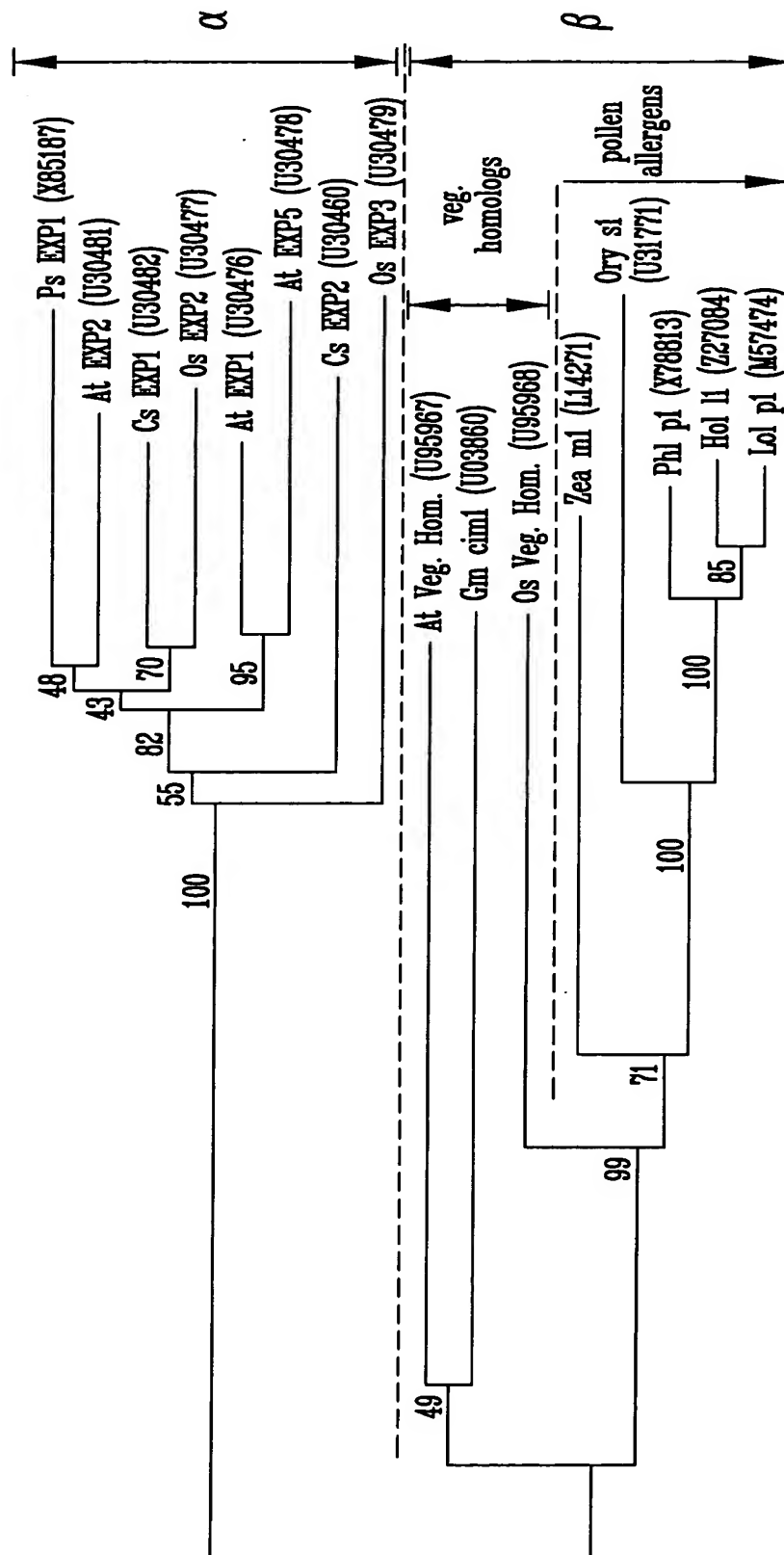


Fig. 4

BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS, COMPOSITIONS THEREOF AND METHODS OF USE

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MASLS - - - - - L - LLVAGSLLAV - LG - CPGPTKVL TGSNITVA - ASDWL Majority
 10 20 30 40 50
 1 V - - - - - FLHLLISGS - - - - - GSTPPLTHSNQQVA - ATRWL z37641.PRO
 1 HGSLANNI - - - - - MVVGAVLAALVVGSGCPPKVPFGPNITTYNGKWL zeamlA.PRO
 1 MASSSSVL - - - - - LVVA - LFAVFLGSAHGIKVPFGPNITAEYGDKWL Lolpl.PRO
 1 MAGASAKV - - - - - V - - - - - AMLLSVLATYGFAGAV - - - - - YTNDDL OsEXPIbeta.PRO
 1 MALT LQRA LSELLT LIAI LSI FLVIP SF C FNPKKLYNASY YSPS - SSDWS ciml.PRO
 1 HTILVVDRY YMLMNL L FAL T C L LNL L TH C F S P K K - F N I S A A T T S - D S D W S beta2 predicted protein.PRC
 1 V - - - - - FLHLLISGS - - - - - GSTPPLTHSNQQVA - ATRWL AtEXPIbeta.PRO
 . A . . TWYG G . G GGACG P G . G Consensus #1
 PATATWYGSPNGAGS - - NGGACGYGKNVDQPPFSGMVGAGSPPLFKDGKG Majority
 60 70 80 90 100
 30 PATA TWYGSAE G D G S - - S GGACGYGSLVDVKP FRKARVGAVSPILFKKGGE z37641.PRO
 45 TARATWYGQPNAGAPDNGGACGI - KNVNLPPYSGMTACGNVPIFKDGKG zeamlA.PRO
 43 DAKSTWYGKPTGAGPKDNGGACGY - KNVNDKAPFNGMTGCGNPIFKDGGRG Lolpl.PRO
 33 PAKATWYGQPNAGAPDNDGGACGF - KNTNQYPFMSMTSCGNEPLFKDGKG OsEXPIbeta.PRO
 50 PAVATWYGPA NG D G S - - E GGACGYGNAV G Q P P F S S L I S A G S P L I Y D S G K G ciml.PRO
 49 IAGSTWYG NPT GY G S - - D GGACGYGNAVAGQPPFSKMVSAGGSPSLFKSGKG beta2 predicted protein.PRC
 30 PATA TWYGSAE G D G S - - S GGACGYGSLVDVKP FRKARVGAVSPILFKKGGE AtEXPIbeta.PRO
 CG . C C CS TD HFDLSG . AFG . Consensus #1
 CGACYEVRCTDKSACSGNPVTVIITDESP - - - SAKAAHYHFDLSGAAPFGA Majority
 110 120 130 140 150
 78 CGAC CYKVR C LDKTI CS KRAVTIIATD QSPSGPSAKAKHTHFDLSGA AFGH z37641.PRO
 94 CGSC CYEVR C KEKPEC CS GNPVTVFI TDMM - - - YEPIAPYHFDLSGKA FGS zeamlA.PRO
 92 CGSC CFEIK C TKPES CS GEAVTVTI TD DN - - - YEPIAPYHFDLSGHA FGS Lolpl.PRO
 82 CGAC CYQIR C TNNPS CS GQPRVTI TD MN - - - YPVARYHFDLSGTA FGA OsEXPIbeta.PRO
 98 CGSC CYEVK C TGN SACS GNPVKVVI TD ECAG - - CGSDAQYHFDLSGNA FGA ciml.PRO
 97 CGAC CYQVK C TSKSACS KNPVTVVI TD ECPG - - CVKESV - HFDLSGTA FGA beta2 predicted protein.PRC
 78 CGAC CYKVR C LDKTI CS KRAVTIIATD QSPSGPSAKAKHTHFDLSGA AFGH AtEXPIbeta.PRO
 . A . . G R . . G C . Y F L . Consensus #1
 MAIPGLNGVLRNAGLLNILFRRVACKYP - GKNIAFHVEAGSNPNYLAVLV Majority
 160 170 180 190 200
 128 MAIP GHNGVIRNRGL LNLILYRRTAC K Y R - GKNIAF H VNAGSTDYWLSL LI z37641.PRO
 140 LAKPG LNDKLRHCG IMDVEFRVRVCKYR PAGQKIVF H IEKGCNPNYVAV LV zeamlA.PRO
 138 MAKKGEEQNVRSAGELELQFRVRVCKYR PDDTKPTF H VEKASNPNYLA ILV Lolpl.PRO
 128 MARPG LNDQLRHAG IIDIQFRVRVCKYR RGLYVNF H VEAGSNPNYLA LV OsEXPIbeta.PRO
 146 MAISG QDENLRNAG KINIQHRIE C N Y I - GR SIAF H VDSGSNQEYFAT LV ciml.PRO
 144 MAISG QDQLRNAG GELQILYKKVE C N Y I - GKT VTF QVDKGSNDYFAVL V beta2 predicted protein.PRC
 128 MAIP GHNGVIRNRGL LNLILYRRTAC K Y R - GKNIAF H VNAGSTDYWLSL LI AtEXPIbeta.PRO
 G W WG W L P . Consensus #1
 EYVDGGDGDIGSMEIKEALGSKE - - - - WISMKQSWGAVWRIDVEGPLKGPFF Majority
 210 220 230 240 250
 177 EYEDGE G D I G S M H I R Q A - G S K E - - - - W I S M K H I W G A N W C I - V E G P L K G P F z37641.PRO
 190 K F V A D D G D I D V L M E I Q D K L S A E - - - - W K P M K L S W G A I W R M D T A K A L K G P F zeamlA.PRO
 188 K Y V D G D G D V V A V D I K E K G K D K - - - - W I E L K E S W G A V W R I D T P D K L T G P F Lolpl.PRO
 177 E F A N K D G D T V V Q L D V M E S L P S G K P T R V W T P M R R S W G S I W R L D A N H R L G Q P X OsEXPIbeta.PRO
 195 E Y E D G D G D L A K V E L K E A L D S G S - - - - W D S M Q Q S W G A V W K F D K G S P L R A P F ciml.PRO
 193 A Y V N G D G E I G R I E L K Q A L D S D K - - - - W L S M S Q S W G A V W K L D V S S P L R A P L beta2 predicted protein.PRC
 177 E Y E D G E G D I G S M H I R Q A - G S K E - - - - W I S M K H I W G A N W C I - V E G P L K G P F AtEXPIbeta.PRO
 SVRLTTLES GKT V I A T D V I P A N W V P D A T Y T S N V N F - - - - Consensus #1
 Majority
 260 270 280 290
 221 SVKLTTLSNNKTL SATDVIPSNWVPKATYTSRLNFSFVL . z37641.PRO
 235 SIRLTS - ESGKKVI AKDIIIPANWRPDAVYTSNVQFY . zeamlA.PRO
 233 TVRYTT - EGGTKSEFEDVIEPGWKADTSYSAK Lolpl.PRO
 227 SLRMVS - ESGQTVIAHQVIPANWRANTNYSKVSQVFR OsEXPIbeta.PRO
 241 SIKLTTTL ciml.PRO
 239 SLRVTSLES GKT V V A S N V I P A N W Q P G A I Y K S N V N F beta2 predicted protein.PRC
 221 SVKLTTLSNNKTL SATDVIPSNWVPKATYTSRLNFSFV - L AtEXPIbeta.PRO

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #1' exactly.

Fig. 5

BETA-EXPANSINS AS CELL WALL LOOSENING AGENTS, COMPOSITIONS THEREOF AND METHODS OF USE

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Consensus #2
Majority

10 20 30 40 50

1 MASSSS--VLLVVALFAVFLGSAHGIAR--VPPGPNITAEYGD--KWL D Lolpl.PRO
1 MAGASAK--VVAAML LSVLATY--GFAAGV-- --YTN--DWL F OsEXPlbeta.PRO
1 MTILVVD--RYYMLMNL LFPALTCLLLHLTHCFSPKKFNISAATTS DSDWS I beta2 predicted protein.PRC
1 V-----FLHLLLSGSGSTPPLTH-----SNQOVAATR WLP ATEXP1beta.PRO
1 NAFSYSPFSSLLFLFPFFVFT-----FADY--GGWQS CuEXPlSIGN.PRO
1 ME--KLPPAFAPFLALSNPFFLPVNA-----FTA--S WAP CuEXPl2sign.PRO
1 MAGSSAATSCARFLALLATCLLWNEA-----ASF TA--SGWNK OsEXPl1.PRO
1 HALV-----TFLIATLGCATSSNNSA-----RDVNGYAG--GWN ATEXP1.PRO

...T.YG...G...GGACG...F...G...C Consensus #2
AHATFYGGPDGSGT M--GGACG YGNLYSQGPF GTHNTAALSTALPHNDGAGC Majority

60 70 80 90 100

44 AKSTWY GKP TGA GPRDN GGACG YKN-VDKAPFNGMTGCGNTPIFI K DGRG K Lolpl.PRO
34 AKATWY GQPN GAG PDDN GGACG FKN-TNQYPPFMSMTSCGNEPLF QDKG K OsEXPlbeta.PRO
50 AGSTWY GNPTGYGS--DGGACG YGNAVAQPPFSK MVSAGG PSLFKS G K beta2 predicted protein.PRC
31 ATATWY GSAEGDGS--SGGACG YGSLVDV KPFKARVGAVSPILFKG GEGC ATEXP1beta.PRO
31 GHATFY GGGDAS G TM--GGACG YGNLYSQG-YGTNTVALSTALPHNGLS C CuEXPlSIGN.PRO
33 AHATFY GESDAS G TM--GGACG YGHL YQTG-YGTRTAALSTALPHNDGAS C CuEXPl2sign.PRO
37 AFATFY GGS'DAS G TH--GGACG YGDLYQTG-YGTNTAALSTVLFNDGAS C OsEXPl1.PRO
34 AHATFY GGGDAS G TM--GGACG YGHL YSQG-YGTNTAALSTALPHNGLS C ATEXP1.PRO

G.C...C...T... Consensus #2
GACFEIR C--TDPKWC--SGTAVTVTATDFC PPHYALFN--GGWCNFF LQ Majority

110 120 130 140 150

93 GACFEIR C--TKPES C--SGRAVTVTIT D DH--BEP--I AFY Lolpl.PRO
83 GACQOIR C--TNHFS C--SGQPRTVIT D MH--YYP--VARY OsEXPlbeta.PRO
98 GACQVVR C--TSKSA C--SKNPVTVIT D ECPGVKES--V--beta2 predicted protein.PRC
79 GACQKVR C--LDKTI C--SKRAVTVIAT DQSPSGPSAK--AKHT ATEXP1beta.PRO
78 GACFEMTC--TSDPKW CLPGT-IRVTATNFCPPFNALPHNNGGWCNFF LQ CuEXPlSIGN.PRO
80 GQC FKIIC DYKATDRFWCIKGASVTITATNFCPPFNALPHNNGGWCNFF LQ CuEXPl2sign.PRO
84 GQC FRIIC DYQADRRFCISGTSVTITATNLCPPFNALPHNAGGWCNPPRQ OsEXPl1.PRO
81 GACFEIR C--QNDGRWC L PGS-IVVTATNFCPPFNALPHNAGGWCNPPRQ ATEXP1.PRO

HFD...G...C...F... Consensus #2
HFDLSGPAFGAIAIYG--RRAGIVFVLYRRVPC KYRGG--VRFTVN-- Majority

160 170 180 190 200

127 HFDLSGHAFGSMARKKEEQNVRSAG E LELQFRVRVC KYPDDTKPT F HVEK Lolpl.PRO
117 HFDLSGTAFGAMARFGLNDLRHAG I IDIQFRVRVC C-YHRGLYVNFHVEA OsEXPlbeta.PRO
133 HFDLSGTAFGAMASIGQDSLNRVAG E LQILYKKVE CNY-IGKT VTFQVDK beta2 predicted protein.PRC
117 HFDLSGAAPGHMAI PGHNGVIRNRG E LNLILYRRTA C KY-RGKNIA FHVNA ATEXP1beta.PRO
125 HFDMAEPFLOIAQY--RAG IVPVSFRRVF CMEKGG--VRFTIN- CuEXPlSIGN.PRO
130 HFDMAQPAWQKIGIY--RG IIPVLYQRVP C KKRGG--VRFTIN- CuEXPl2sign.PRO
134 HFDMAEPAWLKIGVY--VGG IVPVLYQRVP C AKKGG--VRFTIN- OsEXPl1.PRO
128 HFDLSQPVFORIAQY--RAG IVPVAYRRVF C VRRGG--IRFTIN- ATEXP1.PRO

...L...G...W...WG...W... Consensus #2
-GNDYFLLVLVTNVGGAGDVGSVSIK--GSRTG-WISMSRNWGANW- Majority

210 220 230 240 250

177 ASNPNYLA L LKYYVDGD G DVVAVDIRE--KGDK WIELKES WGAVWR Lolpl.PRO
166 GSNPVYLA L LVEFANED G TVVQLDVMSLSPSGKPTRV WTPMRRS WGSIWR OsEXPlbeta.PRO
182 GSNANSAFV L VAYVNGDG E IGRIEHLQAL--DSDK WLSMSQS WGAVWK beta2 predicted protein.PRC
166 GSTDYWLS L LIEYEDGEG E D GSMHIRQA--GSKE WISMKHI WGANW ATEXP1beta.PRO
165 -GHSYFNLV L LITNVGGAG G DVHSVSIK--GSRTG WQMSMRNWGANW- CuEXPlSIGN.PRO
170 -GRDYFBLV L LITNVGGAG G DIKS VSIK--GSKSSN WTPMSRNWGANW- CuEXPl2sign.PRO
174 -GRDYFBLV L LVS NVGGV G SIQSVSIK--GSRTG W MAMSRNWGVNW- OsEXPl1.PRO
168 -GHSYFNLV L LITNVGGAG G DVHSAMVK--GSRTG W QAMSRNWGANW- ATEXP1.PRO

...L...W... Consensus #2
-QSNYSYLNGQPLSFKVTT-SDGQTLVANNVIPANWQFGQTYSSK VQFS-- Majority

260 270 280 290 300

222 IDTPDK L LG-PFTVRYTT-EGGTRKSEFPEDVIPBG W RADTSYSAR Lolpl.PRO
216 LDANHR L LG-PXSLRMVS-ESGQTVIAHQVIPAN W RANTHYGSKVQFR OsEXPlbeta.PRO
228 LDVVSPL L RA-PLSLRVTSLES GKT VVASNVIPAN W QPGAIYKSNVNF beta2 predicted protein.PRC
211 I-VEGFL L KG-PFSVKTLLT LSNKLT SATDVIPSN W VPKATYTSRLNFSFV ATEXP1beta.PRO
207 -QSNYSYL NGQGLSFKVTL-SDGRTLTAYNLVPSN W QFGQTYEGP-QF CuEXPlSIGN.PRO
213 -QSNYSYL NGQGLSFKVTT-SDGQTVQVFNNDVPSN W RFGQTFASKVQFS CuEXPl2sign.PRO
216 -QSNAYL L DGQSLSFKVTS-SDGQTLTFLVDVAPAG W TFGQTFSTSSQQS OsEXPl1.PRO
210 -QSNYSYL L NGQSLSFKVTT-SDGQTVSNVNVANAG W SPFGQTFGTGA-QLR ATEXP1.PRO

Consensus #2
Majority

263
261
273
259 L
250
258
261
254

Lolpl.PRO
OsEXPlbeta.PRO
beta2 predicted protein.PRC
ATEXP1beta.PRO
CuEXPlSIGN.PRO
CuEXPl2sign.PRO
OsEXPl1.PRO
ATEXP1.PRO

Consensus 'Consensus #2': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Fig. 6